

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/584,482
Source: 1FWP
Date Processed by STIC: 7/7/06

ENTERED



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/584,482

DATE: 07/07/2006

TIME: 14:52:51

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\07072006\J584482.raw

3 <110> APPLICANT: HAGIWARA, Masatoshi

5 <120> TITLE OF INVENTION: Method for controlling SR protein phosphorylation, and antiviral agents

6 whose active ingredients comprise agents that control SR protein activity

8 <130> FILE REFERENCE: 6235-76051-01

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/584,482

C--> 11 <141> CURRENT FILING DATE: 2006-06-23

13 <150> PRIOR APPLICATION NUMBER: JP 2003-435085

14 <151> PRIOR FILING DATE: 2003-12-26

16 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/019393

17 <151> PRIOR FILING DATE: 2004-12-24

19 <160> NUMBER OF SEQ ID NOS: 5

21 <170> SOFTWARE: PatentIn version 3.1

23 <210> SEQ ID NO: 1

24 <211> LENGTH: 1965

25 <212> TYPE: DNA

26 <213> ORGANISM: Homo sapiens

28 <220> FEATURE:

29 <221> NAME/KEY: CDS

30 <222> LOCATION: (1)..(1965)

31 <223> OTHER INFORMATION:

W--> 33 <400> 1

34	atg gag cgg aaa gtg ctt gcg ctc cag gcc cga aag aaa agg acc aag	48
35	Met Glu Arg Lys Val Leu Ala Leu Gln Ala Arg Lys Lys Arg Thr Lys	
36	1 5 10 15	
38	gcc aag aag gac aaa gcc caa agg aaa tct gaa act cag cac cga ggc	96
39	Ala Lys Lys Asp Lys Ala Gln Arg Lys Ser Glu Thr Gln His Arg Gly	
40	20 25 30	
42	tct gct ccc cac tct gag agt gat cta cca gag cag gaa gag gag att	144
43	Ser Ala Pro His Ser Glu Ser Asp Leu Pro Glu Gln Glu Glu Glu Ile	
44	35 40 45	
46	ctg gga tct gat gat gat gag caa gaa gat cct aat gat tat tgt aaa	192
47	Leu Gly Ser Asp Asp Asp Glu Gln Glu Asp Pro Asn Asp Tyr Cys Lys	
48	50 55 60	
50	gga ggt tat cat ctt gtg aaa att gga gat cta ttc aat ggg aga tac	240
51	Gly Gly Tyr His Leu Val Lys Ile Gly Asp Leu Phe Asn Gly Arg Tyr	
52	65 70 75 80	
54	cat gtg atc cga aag tta ggc tgg gga cac ttt tca aca gta tgg tta	288
55	His Val Ile Arg Lys Leu Gly Trp Gly His Phe Ser Thr Val Trp Leu	
56	85 90 95	
58	tca tgg gat att cag ggg aag aaa ttt gtg gca atg aaa gta gtt aaa	336
59	Ser Trp Asp Ile Gln Gly Lys Lys Phe Val Ala Met Lys Val Val Lys	
60	100 105 110	

62 agt gct gaa cat tac act gaa aca gca cta gat gaa atc cgg ttg ctg 384

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63	Ser	Ala	Glu	His	Tyr	Thr	Glu	Thr	Ala	Leu	Asp	Glu	Ile	Arg	Leu	Leu	
64			115					120					125				
66	aag	tca	gtt	cgc	aat	tca	gac	cct	aat	gat	cca	aat	aga	gaa	atg	gtt	432
67	Lys	Ser	Val	Arg	Asn	Ser	Asp	Pro	Asn	Asp	Pro	Asn	Arg	Glu	Met	Val	
68		130					135					140					
70	gtt	caa	cta	cta	gat	gac	ttt	aaa	ata	tca	gga	gtt	aat	gga	aca	cat	480
71	Val	Gln	Leu	Leu	Asp	Asp	Phe	Lys	Ile	Ser	Gly	Val	Asn	Gly	Thr	His	
72	145					150					155					160	
74	atc	tgc	atg	gta	ttt	gaa	gtt	ttg	ggg	cat	cat	ctg	ctc	aag	tgg	atc	528
75	Ile	Cys	Met	Val	Phe	Glu	Val	Leu	Gly	His	His	Leu	Leu	Lys	Trp	Ile	
76					165					170					175		
78	atc	aaa	tcc	aat	tat	cag	ggg	ctt	cca	ctg	cct	tgt	gtc	aaa	aaa	att	576
79	Ile	Lys	Ser	Asn	Tyr	Gln	Gly	Leu	Pro	Leu	Pro	Cys	Val	Lys	Lys	Ile	
80				180					185					190			
82	att	cag	caa	gtg	tta	cag	ggg	ctt	gat	tat	tta	cat	acc	aag	tgc	cgt	624
83	Ile	Gln	Gln	Val	Leu	Gln	Gly	Leu	Asp	Tyr	Leu	His	Thr	Lys	Cys	Arg	
84			195					200					205				
86	atc	atc	cac	act	gac	att	aaa	cca	gag	aac	atc	tta	ttg	tca	gtg	aat	672
87	Ile	Ile	His	Thr	Asp	Ile	Lys	Pro	Glu	Asn	Ile	Leu	Leu	Ser	Val	Asn	
88		210					215					220					
90	gag	cag	tac	att	cgg	agg	ctg	gct	gca	gaa	gca	aca	gaa	tgg	cag	cga	720
91	Glu	Gln	Tyr	Ile	Arg	Arg	Leu	Ala	Ala	Glu	Ala	Thr	Glu	Trp	Gln	Arg	
92	225				230						235				240		
94	tct	gga	gct	cct	ccg	cct	tcc	gga	tct	gca	gtc	agt	act	gct	ccc	cag	768
95	Ser	Gly	Ala	Pro	Pro	Pro	Ser	Gly	Ser	Ala	Val	Ser	Thr	Ala	Pro	Gln	
96				245						250				255			
98	cct	aaa	cca	gct	gac	aaa	atg	tca	aag	aat	aag	aag	aag	aaa	ttg	aag	816
99	Pro	Lys	Pro	Ala	Asp	Lys	Met	Ser	Lys	Asn	Lys	Lys	Lys	Lys	Leu	Lys	
100			260						265					270			
102	aag	aag	cag	aag	cgc	cag	gca	gaa	tta	cta	gag	aag	cga	atg	cag	gaa	864
103	Lys	Lys	Gln	Lys	Arg	Gln	Ala	Glu	Leu	Leu	Glu	Lys	Arg	Met	Gln	Glu	
104			275					280					285				
106	att	gag	gaa	atg	gag	aaa	gag	tcg	ggc	cct	ggg	caa	aaa	aga	cca	aac	912
107	Ile	Glu	Glu	Met	Glu	Lys	Glu	Ser	Gly	Pro	Gly	Gln	Lys	Arg	Pro	Asn	
108		290					295					300					
110	aag	caa	gaa	gaa	tca	gag	agt	cct	gtt	gaa	aga	ccc	ttg	aaa	gag	aac	960
111	Lys	Gln	Glu	Glu	Ser	Glu	Ser	Pro	Val	Glu	Arg	Pro	Leu	Lys	Glu	Asn	
112	305					310					315				320		
114	cca	cct	aat	aaa	atg	acc	caa	gaa	aaa	ctt	gaa	gag	tca	agt	acc	att	1008
115	Pro	Pro	Asn	Lys	Met	Thr	Gln	Glu	Lys	Leu	Glu	Glu	Ser	Ser	Thr	Ile	
116				325						330					335		
118	ggc	cag	gat	caa	acg	ctt	atg	gaa	cgt	gat	aca	gag	ggg	ggg	gca	gca	1056
119	Gly	Gln	Asp	Gln	Thr	Leu	Met	Glu	Arg	Asp	Thr	Glu	Gly	Gly	Ala	Ala	
120			340						345					350			
122	gaa	att	aat	tgc	aat	gga	gtg	att	gaa	gtc	att	aat	tat	act	cag	aac	1104
123	Glu	Ile	Asn	Cys	Asn	Gly	Val	Ile	Glu	Val	Ile	Asn	Tyr	Thr	Gln	Asn	
124			355					360					365				
126	agt	aat	aat	gaa	aca	ttg	aga	cat	aaa	gag	gat	cta	cat	aat	gct	aat	1152
127	Ser	Asn	Asn	Glu	Thr	Leu	Arg	His	Lys	Glu	Asp	Leu	His	Asn	Ala	Asn	

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128	370	375	380	
130	gac tgt gat gtc	caa aat ttg aat	cag gaa tct agt ttc	cta agc tcc 1200
131	Asp Cys Asp Val	Gln Asn Leu Asn	Gln Glu Ser Ser	Phe Leu Ser Ser
132	385	390	395	400
134	caa aat gga gac	agc agc aca tct	caa gaa aca gac	tct tgt aca cct 1248
135	Gln Asn Gly Asp	Ser Ser Thr Ser	Gln Glu Thr Asp	Ser Ser Cys Thr Pro
136		405	410	415
138	ata aca tct gag	gtg tca gac acc	atg gtg tgc cag	tct tcc tca act 1296
139	Ile Thr Ser Glu	Val Ser Asp Thr	Met Val Cys Gln	Ser Ser Ser Thr
140		420	425	430
142	gta ggt cag tca	ttc agt gaa caa	cac att agc caa	ctt caa gaa agc 1344
143	Val Gly Gln Ser	Phe Ser Glu Gln	His Ile Ser Gln	Leu Gln Glu Ser
144		435	440	445
146	att cgg gca gag	ata ccc tgt gaa	gat gaa caa gag	caa gaa cat aac 1392
147	Ile Arg Ala Glu	Ile Pro Cys Glu	Asp Glu Gln Gln	Glu Glu His Asn
148		450	455	460
150	gga cca ctg gac	aac aaa gga aaa	tcc acg gct gga	aat ttt ctt gtt 1440
151	Gly Pro Leu Asp	Asn Lys Gly Lys	Ser Thr Ala Gly	Asn Phe Leu Val
152	465	470	475	480
154	aat ccc ctt gag	cca aaa aat gca	gaa aag ctc aag	gtg aag att gct 1488
155	Asn Pro Leu Glu	Pro Lys Asn Ala	Glu Lys Leu Lys	Val Lys Ile Ala
156		485	490	495
158	gac ctt gga aat	gct tgt tgg gtg	cac aaa cat ttc	act gaa gat att 1536
159	Asp Leu Gly Asn	Ala Cys Trp Val	His Lys His Phe	Thr Glu Asp Ile
160		500	505	510
162	caa aca agg caa	tat cgt tcc ttg	gaa gtt cta atc	gga tct ggc tat 1584
163	Gln Thr Arg Gln	Tyr Arg Ser Leu	Glu Val Leu Ile	Gly Ser Gly Tyr
164		515	520	525
166	aat acc cct gct	gac att tgg agc	acg gca tgc atg	gcc ttt gaa ctg 1632
167	Asn Thr Pro Ala	Asp Ile Trp Ser	Thr Ala Cys Met	Ala Phe Glu Leu
168		530	535	540
170	gcc aca ggt gac	tat ttg ttt gaa	cct cat tca ggg	gaa gag tac act 1680
171	Ala Thr Gly Asp	Tyr Leu Phe Glu	Pro His Ser Gly	Glu Glu Tyr Thr
172	545	550	555	560
174	cga gat gaa gat	cac att gca ttg	atc ata gaa ctt	ctg ggg aag gtg 1728
175	Arg Asp Glu Asp	His Ile Ala Leu	Ile Ile Glu Leu	Leu Gly Lys Val
176		565	570	575
178	cct cgc aag ctc	att gtg gca gga	aaa tat tcc aag	gaa ttt ttc acc 1776
179	Pro Arg Lys Leu	Ile Val Ala Gly	Lys Tyr Ser Lys	Glu Phe Phe Thr
180		580	585	590
182	aaa aaa ggt gac	ctg aaa cat atc	acg aag ctg aaa	cct tgg ggc ctt 1824
183	Lys Lys Gly Asp	Leu Lys His Ile	Thr Lys Leu Lys	Pro Trp Gly Leu
184		595	600	605
186	ttt gag gtt cta	gtg gag aag tat	gag tgg tcg cag	gaa gag gca gct 1872
187	Phe Glu Val Leu	Val Glu Lys Tyr	Glu Trp Ser Gln	Glu Glu Ala Ala
188		610	615	620
190	ggc ttc aca gat	ttc tta ctg ccc	atg ttg gag ctg	atc cct gag aag 1920
191	Gly Phe Thr Asp	Phe Leu Pro Met	Leu Glu Leu Ile	Pro Glu Lys
192	625	630	635	640

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194 aga gcc act gcc gcc gag tgt ctc cgg cac cct tgg ctt aac tcc      1965
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196                645                650                655
199 <210> SEQ ID NO: 2
200 <211> LENGTH: 655
201 <212> TYPE: PRT
202 <213> ORGANISM: Homo sapiens
204 <400> SEQUENCE: 2
205 Met Glu Arg Lys Val Leu Ala Leu Gln Ala Arg Lys Lys Arg Thr Lys
206 1                5                10                15
208 Ala Lys Lys Asp Lys Ala Gln Arg Lys Ser Glu Thr Gln His Arg Gly
209                20                25                30
211 Ser Ala Pro His Ser Glu Ser Asp Leu Pro Glu Gln Glu Glu Ile
212                35                40                45
214 Leu Gly Ser Asp Asp Asp Glu Gln Glu Asp Pro Asn Asp Tyr Cys Lys
215 50                55                60
217 Gly Gly Tyr His Leu Val Lys Ile Gly Asp Leu Phe Asn Gly Arg Tyr
218 65                70                75                80
220 His Val Ile Arg Lys Leu Gly Trp Gly His Phe Ser Thr Val Trp Leu
221                85                90                95
223 Ser Trp Asp Ile Gln Gly Lys Lys Phe Val Ala Met Lys Val Val Lys
224                100               105               110
226 Ser Ala Glu His Tyr Thr Glu Thr Ala Leu Asp Glu Ile Arg Leu Leu
227                115               120               125
229 Lys Ser Val Arg Asn Ser Asp Pro Asn Asp Pro Asn Arg Glu Met Val
230                130               135               140
232 Val Gln Leu Leu Asp Asp Phe Lys Ile Ser Gly Val Asn Gly Thr His
233 145               150               155               160
235 Ile Cys Met Val Phe Glu Val Leu Gly His His Leu Leu Lys Trp Ile
236                165               170               175
238 Ile Lys Ser Asn Tyr Gln Gly Leu Pro Leu Pro Cys Val Lys Lys Ile
239                180               185               190
241 Ile Gln Gln Val Leu Gln Gly Leu Asp Tyr Leu His Thr Lys Cys Arg
242                195               200               205
244 Ile Ile His Thr Asp Ile Lys Pro Glu Asn Ile Leu Leu Ser Val Asn
245                210               215               220
247 Glu Gln Tyr Ile Arg Arg Leu Ala Ala Glu Ala Thr Glu Trp Gln Arg
248 225               230               235               240
250 Ser Gly Ala Pro Pro Pro Ser Gly Ser Ala Val Ser Thr Ala Pro Gln
251                245               250               255
253 Pro Lys Pro Ala Asp Lys Met Ser Lys Asn Lys Lys Lys Lys Leu Lys
254                260               265               270
256 Lys Lys Gln Lys Arg Gln Ala Glu Leu Leu Glu Lys Arg Met Gln Glu
257                275               280               285
259 Ile Glu Glu Met Glu Lys Glu Ser Gly Pro Gly Gln Lys Arg Pro Asn
260                290               295               300
262 Lys Gln Glu Glu Ser Glu Ser Pro Val Glu Arg Pro Leu Lys Glu Asn
263 305               310               315               320
265 Pro Pro Asn Lys Met Thr Gln Glu Lys Leu Glu Glu Ser Ser Thr Ile

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266          325          330          335
268 Gly Gln Asp Gln Thr Leu Met Glu Arg Asp Thr Glu Gly Gly Ala Ala
269          340          345          350
271 Glu Ile Asn Cys Asn Gly Val Ile Glu Val Ile Asn Tyr Thr Gln Asn
272          355          360          365
274 Ser Asn Asn Glu Thr Leu Arg His Lys Glu Asp Leu His Asn Ala Asn
275          370          375          380
277 Asp Cys Asp Val Gln Asn Leu Asn Gln Glu Ser Ser Phe Leu Ser Ser
278 385          390          395          400
280 Gln Asn Gly Asp Ser Ser Thr Ser Gln Glu Thr Asp Ser Cys Thr Pro
281          405          410          415
283 Ile Thr Ser Glu Val Ser Asp Thr Met Val Cys Gln Ser Ser Ser Thr
284          420          425          430
286 Val Gly Gln Ser Phe Ser Glu Gln His Ile Ser Gln Leu Gln Glu Ser
287          435          440          445
289 Ile Arg Ala Glu Ile Pro Cys Glu Asp Glu Gln Glu Gln Glu His Asn
290          450          455          460
292 Gly Pro Leu Asp Asn Lys Gly Lys Ser Thr Ala Gly Asn Phe Leu Val
293 465          470          475          480
295 Asn Pro Leu Glu Pro Lys Asn Ala Glu Lys Leu Lys Val Lys Ile Ala
296          485          490          495
298 Asp Leu Gly Asn Ala Cys Trp Val His Lys His Phe Thr Glu Asp Ile
299          500          505          510
301 Gln Thr Arg Gln Tyr Arg Ser Leu Glu Val Leu Ile Gly Ser Gly Tyr
302          515          520          525
304 Asn Thr Pro Ala Asp Ile Trp Ser Thr Ala Cys Met Ala Phe Glu Leu
305          530          535          540
307 Ala Thr Gly Asp Tyr Leu Phe Glu Pro His Ser Gly Glu Glu Tyr Thr
308 545          550          555          560
310 Arg Asp Glu Asp His Ile Ala Leu Ile Ile Glu Leu Leu Gly Lys Val
311          565          570          575
313 Pro Arg Lys Leu Ile Val Ala Gly Lys Tyr Ser Lys Glu Phe Phe Thr
314          580          585          590
316 Lys Lys Gly Asp Leu Lys His Ile Thr Lys Leu Lys Pro Trp Gly Leu
317          595          600          605
319 Phe Glu Val Leu Val Glu Lys Tyr Glu Trp Ser Gln Glu Glu Ala Ala
320          610          615          620
322 Gly Phe Thr Asp Phe Leu Leu Pro Met Leu Glu Leu Ile Pro Glu Lys
323 625          630          635          640
325 Arg Ala Thr Ala Ala Glu Cys Leu Arg His Pro Trp Leu Asn Ser
326          645          650          655
329 <210> SEQ ID NO: 3
330 <211> LENGTH: 2058
331 <212> TYPE: DNA
332 <213> ORGANISM: Homo sapiens
334 <220> FEATURE:
335 <221> NAME/KEY: CDS
336 <222> LOCATION: (1)..(2058)
337 <223> OTHER INFORMATION:

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5

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L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:33 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:31
L:339 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:337